dbMHC Resource

NEW

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The dbMHC database provides an open, publicly accessible platform for DNA, and clinical data related to the human Major Histocompatibilty Complex (MHC). The need to share research and clinical data focused on the MHC has lead to a series of meetings at the International HLA WorkShop & Congress (IHWC). The data generated from the 13th IHWC has been made available in dbMHC. In addition the dbMHC will provide tools for further submission and analysis of research data linked to the MHC. Users can access dbMHC at: *www.ncbi.nlm.nih.gov/mhc/MHC.cgi?cmd=init*

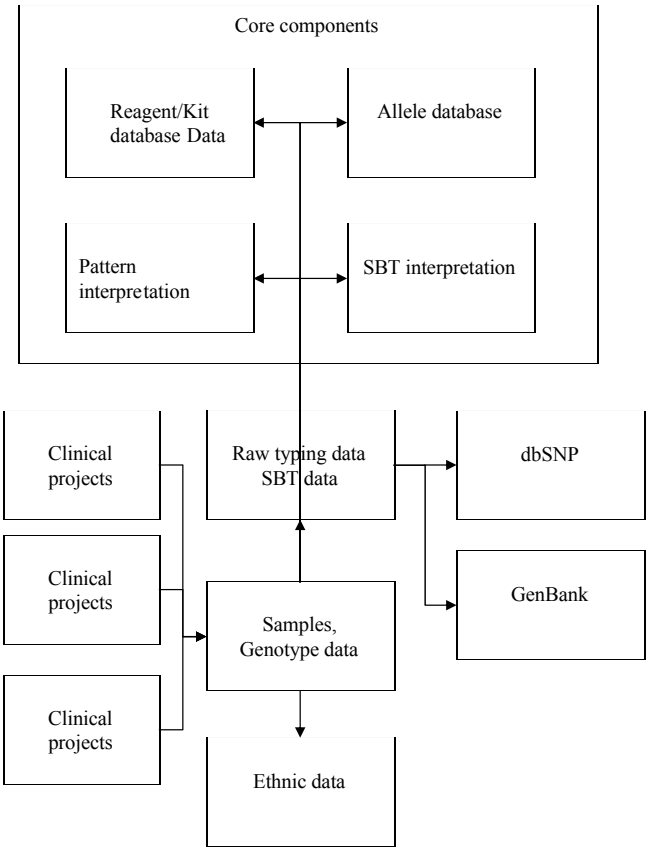
The dbMHC Web pages are divided into two main sections. The Reagent db, currently in beta testing as a prototype, contains the reagent data needed to trace actual DNA typing. This section provides an open platform for the submission, evaluation and editing of individual reagent specifications of Sequence Specific Oligonucleotides (SSO) and Sequence Specific Primers (SSP) as well as typing kit information. All reagents will be characterized for allele specificity using the current curated World Health Organization HLA allele database in cooperation with IMGT/HLA.

The second section will contain anonymous clinical data from individuals taking part in MHC-related research projects in the general categories of Anthropology, Cytokine Polymorphisms, HLA-E,F,G, Cancer, Disease , HLA Alloantibodies & Kidney Graft Rejection, Mycobacterial Disease, New Allele Registry, Hemochromatosis/Psoriasis, and Virtual DNA Analysis.

The data for these projects will be made available following the 13th IHWC.

Please submit questions and comments to the dbMHC staff: Wolfgang Helmberg, helmberg@ncbi.nlm.nih.gov; Michael Feolo, feolo@ncbi.nlm.nih.gov; and Raymond Dunivin, dunivin@ncbi.nlm.nih.gov

Architecture of dbMHC



Description of some tools from the dbMHC

Alignment viewer

An interactive viewer of sequence alignments. An arbitrary combination of sequences can be compared to a reference sequence. Alignments can be displayed either as DNA or as protein alignments.

DNA typing reagent database

A global resource for registration and characterization of DNA typing reagents. It is intended to provide central documentation of DNA typing reagents used world wide. Each reagent is uniquely identified. SSO, SSO mixes, SSP and SSP mixes are supported. The linked tool helps to predict allele reactivities of each type of reagent based on a variable annealing stringency. Individual allele reactivities can be added and deleted independently of the prediction algorithm. Batch submissions in XML format are supported. Recalculation of allele reactivities is performed in synchronization with the IMGT/HLA database.

DNA typing kit database

Reagents registered in the reagent database are grouped in typing kits and each kit or kit batch is uniquely identified. Group-specific amplification of alleles can be specified for an entire kit of sections from each kit. Kits designed to test multiple loci are supported. Kits can be entered and updated via the web or submitted as batches in XML format. HLA DNA typings based on kits in the database can be analysed with an online typing pattern interpretation tool. Analysis can be performed with an arbitrary number of false positive/negative reactivities within each typing result. Probe sequences and their alignments can be displayed at any time.

Both the reagent database and the typing kit database have been designed to facilitate exchange of HLA typing based on raw typing data. Utilizing the unique Identifiers of kits or reagents, batchwise reinterpretation of previous typing data can be performed either at the NCBI or locally with the help of the downloaded allele reactivity lists. Reinterpretation at the NCBI requires submission of raw typing data in XML format.

Sequence Based Typing tool

Heterozygote or allele sequences can be interpreted based on the current allele database. Alignment is based on BLAST. Introns are cut and removed based on the alignment. Heterozygote sequences of alleles with insertions/deletions relative to each other can be analyzed. Analysis can be performed with an arbitrary number of nucleotide mismatches. Insertions/deletions of the query sequences relative to the main alignment are listed in the results page. Mismatch positions are highlighted in the alignment viewer.

The allele database is based on the IMGT/HLA database and currently consists of classical HLA loci, non classical HLA loci and Killer Cell Immunoglobulin-like Receptor loci. However, additional polymorphic loci of interest can be included on request.

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revised 05/2003